

RAW SEQUENCE LISTING
PATENT APPLICATION US/08/154,019DATE: 03/25/97
TIME: 09:16:41

INPUT SET: S16463.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

#26

140

3-27-97

SEQUENCE LISTING

- 1
2
3 (1) General Information:
4
5 (i) APPLICANT: Deboer, Herman A.
6 Strijker, Rein
7 Heyneker, Herbert L.
8 Platenburg, Gerald
9 Lee, Sang He
10 Pieper, Frank
11 Krimpenfort, Paul J.A.
12
13 (ii) TITLE OF INVENTION: Production of Recombinant Polypeptides
14 by Bovine Species and Transgenic Methods
15
16 (iii) NUMBER OF SEQUENCES: 38
17
18 (iv) CORRESPONDENCE ADDRESS:
19 (A) ADDRESSEE: Townsend and Townsend and Crew
20 (B) STREET: One Market Plaza, Steuart Tower, Suite 2000
21 (C) CITY: San Francisco
22 (D) STATE: California
23 (E) COUNTRY: USA
24 (F) ZIP: 94105
25
26 (v) COMPUTER READABLE FORM:
27 (A) MEDIUM TYPE: Floppy disk
28 (B) COMPUTER: IBM PC compatible
29 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
30 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
31
32 (vi) CURRENT APPLICATION DATA:
33 (A) APPLICATION NUMBER: 08/154,019
34 (B) FILING DATE: 16-NOV-1993
35 (C) CLASSIFICATION: 435
36
37 (vii) PRIOR APPLICATION DATA:
38 (A) APPLICATION NUMBER: US 08/461,333
39 (B) FILING DATE: 05-JUN-1995
40
41 (A) APPLICATION NUMBER: US 08/077,788
42 (B) FILING DATE: 15-JUN-1993
43
44 (viii) PRIOR APPLICATION DATA:
45 (A) APPLICATION NUMBER: US 07/895,956
46 (B) FILING DATE: 15-JUN-1992

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47
48 (vii) PRIOR APPLICATION DATA:
49 (A) APPLICATION NUMBER: US 07/619,131
50 (B) FILING DATE: 27-NOV-1990
51
52 (vii) PRIOR APPLICATION DATA:
53 (A) APPLICATION NUMBER: US 07/444,745
54 (B) FILING DATE: 01-DEC-1989
55
56 (viii) ATTORNEY/AGENT INFORMATION:
57 (A) NAME: Liebescheutz, Joe O.
58 (B) REGISTRATION NUMBER: 37,505
59 (C) REFERENCE/DOCKET NUMBER: 16994-003123
60
61 (ix) TELECOMMUNICATION INFORMATION:
62 (A) TELEPHONE: 415-543-9600
63 (B) TELEFAX: 415-543-5043
64
65
66 (2) INFORMATION FOR SEQ ID NO:1:
67
68 (i) SEQUENCE CHARACTERISTICS:
69 (A) LENGTH: 2319 base pairs
70 (B) TYPE: nucleic acid
71 (C) STRANDEDNESS: single
72 (D) TOPOLOGY: linear
73
74 (ii) MOLECULE TYPE: DNA (genomic)
75
76
77 (ix) FEATURE:
78 (A) NAME/KEY: sig_peptide
79 (B) LOCATION: 1..54
80
81 (ix) FEATURE:
82 (A) NAME/KEY: mat_peptide
83 (B) LOCATION: 55..2130
84
85 (ix) FEATURE:
86 (A) NAME/KEY: CDS
87 (B) LOCATION: 1..2130
88
89
90 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
91
92 GGA CTT GTC TTC CTC GTC CTG CTG TTC CTC GGG GCC CTC GGA CTG TGT 48
93 Gly Leu Val Phe Leu Val Leu Leu Phe Leu Gly Ala Leu Gly Leu Cys
94 -18 -15 -10 -5
95
96 CTG GCT GGC CGT AGG AGA AGG AGT GTT CAG TGG TGC GCC GTA TCC CAA 96
97 Leu Ala Gly Arg Arg Arg Arg Ser Val Gln Trp Cys Ala Val Ser Gln
98 1 5 10
99

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100	CCC GAG GCC ACA AAA TGC TTC CAA TGG CAA AGG AAT ATG AGA AAA GTG	144
101	Pro Glu Ala Thr Lys Cys Phe Gln Trp Gln Arg Asn Met Arg Lys Val	
102	15 20 25 30	
103		
104	CTG GGC CCT CCT GTC AGC TGC ATA AAG AGA GAC TCC CCC ATC CAG TGT	192
105	Leu Gly Pro Pro Val Ser Cys Ile Lys Arg Asp Ser Pro Ile Gln Cys	
106	35 40 45	
107		
108	ATC CAG GCC ATT GCG GAA AAC AGG GCC GAT GCT GTG ACC CTT GAT GGT	240
109	Ile Gln Ala Ile Ala Glu Asn Arg Ala Asp Ala Val Thr Leu Asp Gly	
110	50 55 60	
111		
112	GGT TTC ATA TAC GAG GCA GGC CTG GCC CCC TAC AAA CTG CGA CCT GTA	288
113	Gly Phe Ile Tyr Glu Ala Gly Leu Ala Pro Tyr Lys Leu Arg Pro Val	
114	65 70 75	
115		
116	GCG GCG GAA GTC TAC GGG ACC GAA AGA CAG CCA CGA ACT CAC TAT TAT	336
117	Ala Ala Glu Val Tyr Gly Thr Glu Arg Gln Pro Arg Thr His Tyr Tyr	
118	80 85 90	
119		
120	CGG GTG GCT GTG GTG AAG AAG GGC GGC AGC TTT CAG CTG AAC GAA CTG	384
121	Arg Val Ala Val Val Lys Lys Gly Gly Ser Phe Gln Leu Asn Glu Leu	
122	95 100 105 110	
123		
124	CAA GGT CTG AAG TCC TGC CAC ACA GGC CTT CGC AGG ACC GCT GGA TGG	432
125	Gln Gly Leu Lys Ser Cys His Thr Gly Leu Arg Arg Thr Ala Gly Trp	
126	115 120 125	
127		
128	AAT GTC CCT ACA GGG ACA CTT CGT CCA TTC TTG AAT TGG ACG GGT CCA	480
129	Asn Val Pro Thr Gly Thr Leu Arg Pro Phe Leu Asn Trp Thr Gly Pro	
130	130 135 140	
131		
132	CCT GAG CCC ATT GAG GCA GCT GTG CAG TTC TTC TCA GCC AGC TGT GTT	528
133	Pro Glu Pro Ile Glu Ala Ala Val Gln Phe Phe Ser Ala Ser Cys Val	
134	145 150 155	
135		
136	CCC GGT GCA GAT AAA GGA CAG TTC CCC AAC CTG TGT CGC CTG TGT GCG	576
137	Pro Gly Ala Asp Lys Gly Gln Phe Pro Asn Leu Cys Arg Leu Cys Ala	
138	160 165 170	
139		
140	GGG ACA GGG GAA AAC AAA TGT GCC TTC TCC TCC CAG GAA CCG TAC TTC	624
141	Gly Thr Gly Glu Asn Lys Cys Ala Phe Ser Ser Gln Glu Pro Tyr Phe	
142	175 180 185 190	
143		
144	AGC TAC TCT GGT GCC TTC AAG TGT CTG AGA GAC GGG GCT GGA GAC GTG	672
145	Ser Tyr Ser Gly Ala Phe Lys Cys Leu Arg Asp Gly Ala Gly Asp Val	
146	195 200 205	
147		
148	GCT TTT ATC AGA GAG AGC ACA GTG TTT GAG GAC CTG TCA GAC GAG GCT	720
149	Ala Phe Ile Arg Glu Ser Thr Val Phe Glu Asp Leu Ser Asp Glu Ala	
150	210 215 220	
151		
152	GAA AGG GAC GAG TAT GAG TTA CTC TGC CCA GAC AAC ACT CGG AAG CCA	768

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153	Glu	Arg	Asp	Glu	Tyr	Glu	Leu	Leu	Cys	Pro	Asp	Asn	Thr	Arg	Lys	Pro	
154			225					230					235				
155																	
156	GTG	GAC	AAG	TTC	AAA	GAC	TGC	CAT	CTG	GCC	CGG	GTC	CCT	TCT	CAT	GCC	816
157	Val	Asp	Lys	Phe	Lys	Asp	Cys	His	Leu	Ala	Arg	Val	Pro	Ser	His	Ala	
158		240					245					250					
159																	
160	GTT	GTG	GCA	CGA	AGT	GTG	AAT	GGC	AAG	GAG	GAT	GCC	ATC	TGG	AAT	CTT	864
161	Val	Val	Ala	Arg	Ser	Val	Asn	Gly	Lys	Glu	Asp	Ala	Ile	Trp	Asn	Leu	
162		255					260				265				270		
163																	
164	CTC	CGC	CAG	GCA	CAG	GAA	AAG	TTT	GGA	AAG	GAC	AAG	TCA	CCG	AAA	TTC	912
165	Leu	Arg	Gln	Ala	Gln	Glu	Lys	Phe	Gly	Lys	Asp	Lys	Ser	Pro	Lys	Phe	
166					275					280					285		
167																	
168	CAG	CTC	TTT	GGC	TCC	CCT	AGT	GGG	CAG	AAA	GAT	CTG	CTG	TTC	AAG	GAC	960
169	Gln	Leu	Phe	Gly	Ser	Pro	Ser	Gly	Gln	Lys	Asp	Leu	Leu	Phe	Lys	Asp	
170				290					295					300			
171																	
172	TCT	GCC	ATT	GGG	TTT	TCG	AGG	GTG	CCC	CCG	AGG	ATA	GAT	TCT	GGG	CTG	1008
173	Ser	Ala	Ile	Gly	Phe	Ser	Arg	Val	Pro	Pro	Arg	Ile	Asp	Ser	Gly	Leu	
174			305					310					315				
175																	
176	TAC	CTT	GGC	TCC	GGC	TAC	TTC	ACT	GCC	ATC	CAG	AAC	TTG	AGG	AAA	AGT	1056
177	Tyr	Leu	Gly	Ser	Gly	Tyr	Phe	Thr	Ala	Ile	Gln	Asn	Leu	Arg	Lys	Ser	
178		320					325					330					
179																	
180	GAG	GAG	GAA	GTG	GCT	GCC	CGG	CGT	GCG	CGG	GTC	GTG	TGG	TGT	GCG	GTG	1104
181	Glu	Glu	Glu	Val	Ala	Ala	Arg	Arg	Ala	Arg	Val	Val	Trp	Cys	Ala	Val	
182		335				340					345				350		
183																	
184	GGC	GAG	CAG	GAG	CTG	CGC	AAG	TGT	AAC	CAG	TGG	AGT	GGC	TTG	AGC	GAA	1152
185	Gly	Glu	Gln	Glu	Leu	Arg	Lys	Cys	Asn	Gln	Trp	Ser	Gly	Leu	Ser	Glu	
186					355					360					365		
187																	
188	GGC	AGC	GTG	ACC	TGC	TCC	TCG	GCC	TCC	ACC	ACA	GAG	GAC	TGC	ATC	GCC	1200
189	Gly	Ser	Val	Thr	Cys	Ser	Ser	Ala	Ser	Thr	Thr	Glu	Asp	Cys	Ile	Ala	
190				370					375					380			
191																	
192	CTG	GTG	CTG	AAA	GGA	GAA	GCT	GAT	GCC	ATG	AGT	TTG	GAT	GGA	GGA	TAT	1248
193	Leu	Val	Leu	Lys	Gly	Glu	Ala	Asp	Ala	Met	Ser	Leu	Asp	Gly	Gly	Tyr	
194			385					390					395				
195																	
196	GTG	TAC	ACT	GCA	TGC	AAA	TGT	GGT	TTG	GTG	CCT	GTC	CTG	GCA	GAG	AAC	1296
197	Val	Tyr	Thr	Ala	Cys	Lys	Cys	Gly	Leu	Val	Pro	Val	Leu	Ala	Glu	Asn	
198		400					405					410					
199																	
200	TAC	AAA	TCC	CAA	CAA	AGC	AGT	GAC	CCT	GAT	CCT	AAC	TGT	GTG	GAT	AGA	1344
201	Tyr	Lys	Ser	Gln	Gln	Ser	Ser	Asp	Pro	Asp	Pro	Asn	Cys	Val	Asp	Arg	
202		415				420				425					430		
203																	
204	CCT	GTG	GAA	GGA	TAT	CTT	GCT	GTG	GCG	GTG	GTT	AGG	AGA	TCA	GAC	ACT	1392
205	Pro	Val	Glu	Gly	Tyr	Leu	Ala	Val	Ala	Val	Val	Arg	Arg	Ser	Asp	Thr	

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	435	440	445	
206				
207				
208	AGC CTT ACC TGG AAC TCT GTG AAA GGC AAG AAG TCC TGC CAC ACC GCC			1440
209	Ser Leu Thr Trp Asn Ser Val Lys Gly Lys Lys Ser Cys His Thr Ala			
210	450	455	460	
211				
212	GTG GAC AGG ACT GCA GGC TGG AAT ATC CCC ATG GGC CTG CTC TTC AAC			1488
213	Val Asp Arg Thr Ala Gly Trp Asn Ile Pro Met Gly Leu Leu Phe Asn			
214	465	470	475	
215				
216	CAG ACG GGC TCC TGC AAA TTT GAT GAA TAT TTC AGT CAA AGC TGT GCC			1536
217	Gln Thr Gly Ser Cys Lys Phe Asp Glu Tyr Phe Ser Gln Ser Cys Ala			
218	480	485	490	
219				
220	CCT GGG TCT GAC CCG AGA TCT AAT CTC TGT GCT CTG TGT ATT GGC GAC			1584
221	Pro Gly Ser Asp Pro Arg Ser Asn Leu Cys Ala Leu Cys Ile Gly Asp			
222	495	500	505	510
223				
224	GAG CAG GGT GAG AAT AAG TGC GTG CCC AAC AGC AAT GAG AGA TAC TAC			1632
225	Glu Gln Gly Glu Asn Lys Cys Val Pro Asn Ser Asn Glu Arg Tyr Tyr			
226	515	520	525	
227				
228	GGC TAC ACT GGG GCT TTC CGG TGC CTG GCT GAG AAT GCT GGA GAC GTT			1680
229	Gly Tyr Thr Gly Ala Phe Arg Cys Leu Ala Glu Asn Ala Gly Asp Val			
230	530	535	540	
231				
232	GCA TTT GTG AAA GAT GTC ACT GTC TTG CAG AAC ACT GAT GGA AAT AAC			1728
233	Ala Phe Val Lys Asp Val Thr Val Leu Gln Asn Thr Asp Gly Asn Asn			
234	545	550	555	
235				
236	AAT GAG GCA TGG GCT AAG GAT TTG AAG CTG GCA GAC TTT GCG CTG CTG			1776
237	Asn Glu Ala Trp Ala Lys Asp Leu Lys Leu Ala Asp Phe Ala Leu Leu			
238	560	565	570	
239				
240	TGC CTC GAT GGC AAA CGG AAG CCT GTG ACT GAG GCT AGA AGC TGC CAT			1824
241	Cys Leu Asp Gly Lys Arg Lys Pro Val Thr Glu Ala Arg Ser Cys His			
242	575	580	585	590
243				
244	CTT GCC ATG GCC CCG AAT CAT GCC GTG GTG TCT CGG ATG GAT AAG GTG			1872
245	Leu Ala Met Ala Pro Asn His Ala Val Val Ser Arg Met Asp Lys Val			
246	595	600	605	
247				
248	GAA CGC CTG AAA CAG GTG CTG CTC CAC CAA CAG GCT AAA TTT GGG AGA			1920
249	Glu Arg Leu Lys Gln Val Leu Leu His Gln Gln Ala Lys Phe Gly Arg			
250	610	615	620	
251				
252	AAT GGA TCT GAC TGC GCG GAC AAG TTT TGC TTA TTC CAG TCT GAA ACC			1968
253	Asn Gly Ser Asp Cys Pro Asp Lys Phe Cys Leu Phe Gln Ser Glu Thr			
254	625	630	635	
255				
256	AAA AAC CTT CTG TTC AAT GAC AAC ACT GAG TGT CTG GCC AGA CTC CAT			2016
257	Lys Asn Leu Leu Phe Asn Asp Asn Thr Glu Cys Leu Ala Arg Leu His			
258	640	645	650	

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SEQUENCE VERIFICATION REPORT

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Original Text